

7. SEQUENCE LISTING

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(1) GENERAL INFORMATION:

(i) APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen
Sthanam, Narayana
Symersky, Jindrich

(ii) TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE

(iii) NUMBER OF SEQUENCES: 8

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Arnold, White & Durkee
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(C) CITY: Houston
(D) STATE: Texas
(E) COUNTRY: U.S.
(F) ZIP: 77210

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US Unknown
(B) FILING DATE: Concurrently Herewith
(C) CLASSIFICATION: Unknown

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/017,678
(B) FILING DATE: 16-MAY-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Kitchell, Barbara S.
(B) REGISTRATION NUMBER: 33,928
(C) REFERENCE/DOCKET NUMBER: TAMK:193

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (512) 418-3000
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATAACATCTG GGAATAAATC AACGAATGTT ACGGTTTCATA AAAGTGAAGC GGGAAACAAGT 60
AGTGTTTTCT ATTATAAAAC GGGAGATATG CTACCAGAAG ATACGACACA TGTACGATGG 120
TTTTTAAATA TTAACAATGA AAAAAGTTAT GTATCGAAAG ATATTACTAT AAAGGATCAG 180
ATTCAAGGTG GACAGCAGTT AGATTTAAGC ACATTAAACA TTAATGTGAC AGGTACACAT 240
AGCAATTATT ATAGTGGACA AAGTGCAATT ACTGATTTTG AAAAAGCCTT TCCAGGTTCT 300
AAAATAACTG TTGATAATAC GAAGAACACA ATTGATGTAA CAATTCCACA AGGCTATGGG 360
TCATATAATA GTTTTTCAAT TAACTACAAA ACCAAAATTA CGAATGAACA GCAAAAAGAG 420
TTTGTTAATA ATTCACAAGC T 441

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Arg Gly Ser His His His His His His Gly Ser Ile Thr Ser Gly
1 5 10 15
Asn Lys Ser Thr Asn Val Thr Val His Lys Ser Glu Ala Gly Thr Ser
20 25 30
Ser Val Phe Tyr Tyr Lys Thr Gly Asp Met Leu Pro Glu Asp Thr Thr
35 40 45
His Val Arg Trp Phe Leu Asn Ile Asn Asn Glu Lys Ser Tyr Val Ser
50 55 60
Lys Asp Ile Thr Ile Lys Asp Gln Ile Gln Gly Gly Gln Gln Leu Asp
65 70 75 80
Leu Ser Thr Leu Asn Ile Asn Val Thr Gly Thr His Ser Asn Tyr Tyr
85 90 95

Ser Gly Gln Ser Ala Ile Thr Asp Phe Glu Lys Ala Phe Pro Gly Ser
100 105 110

Lys Ile Thr Val Asp Asn Thr Lys Asn Thr Ile Asp Val Thr Ile Pro
115 120 125

Gln Gly Tyr Gly Ser Tyr Asn Ser Phe Ser Ile Asn Tyr Lys Thr Lys
130 135 140

Ile Thr Asn Glu Gln Gln Lys Glu Phe Val Asn Asn Ser Gln Ala
145 150 155

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GACGATAAAA ATGGAAAAAT ACAAATGGT GACATGATTA AAGTGGCATG GCCGACAAGC	60
GGTACAGTAA AGATAGAGGG TTATAGTAAA ACAGTACCAT TAACTGTTAA AGGTGAACAG	120
GTGGGTCAAG CAGTTATTAC ACCAGACGGT GCAACAATTA CATTCAATGA TAAAGTAGAA	180
AAATTAAGTG ATGTTTCGGG ATTTGCAGAA TTTGAAGTAC AAGGAAGAAA TTTAACGCAA	240
ACAAATACTT CAGATGACAA AGTAGCTACG ATAACATCTG GGAATAAATC AACGAATGTT	300
ACGGTTCATA AAAGTGAAGC GGAACAAGT AGTGTTTTCT ATTATAAAAC GGGAGATATG	360
CTACCAGAAG ATACGACACA TGTACGATGG TTTTAAATA TTAACAATGA AAAAAGTTAT	420
GTATCGAAAG ATATTACTAT AAAGGATCAG ATTCAAGGTG GACAGCAGTT AGATTTAAGC	480
ACATTAAACA TTAATGTGAC AGGTACACAT AGCAATTATT ATAGTGGACA AAGTGCAATT	540
ACTGATTTTG AAAAAGCCTT TCCAGGTCT AAAATACTG TTGATAATAC GAAGAACACA	600
ATTGATGTAA CAATTCCACA AGGCTATGGG TCATATAATA GTTTTCAAT TAACTACAAA	660
ACCAAAATTA CGAATGAACA GCAAAAAGAG TTTGTTAATA ATCACAAGC TTGGTATCAA	720
GAGCATGGTA AGGAAGAAGT GAACGGGAAA TCATTTAATC ATACTGTGCA CAATATTAAT	780
GCTAATGCCG GTATTGAAGG TACTGTAAAA GGTGAATTAA AAGTTTTAAA ACAGGATAAA	840
GATACCAAG	849

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Arg Gly Ser His His His His His His Gly [Ser Asp Asp Lys Val
1 5 10 15

Ala Thr Ile Thr Ser Gly Asn Lys Ser Thr Asn Val Thr Val His Lys
20 25 30

Ser Glu Ala Gly Thr Ser Ser Val Phe Tyr Tyr Lys Thr Gly Asp Met
35 40 45

Leu Pro Glu Asp Thr Thr His Val Arg Trp Phe Leu Asn Ile Asn Asn
50 55 60

Glu Lys Ser Tyr Val Ser Lys Asp Ile Thr Ile Lys Asp Gln Ile Gln
65 70 75 80

Gly Gly Gln Gln Leu Asp Leu Ser Thr Leu Asn Ile Asn Val Thr Gly
85 90 95

Thr His Ser Asn Tyr Tyr Ser Gly Gln Ser Ala Ile Thr Asp Phe Glu
100 105 110

Lys Ala Phe Pro Gly Ser Lys Ile Thr Val Asp Asn Thr Lys Asn Thr
115 120 125

Ile Asp Val Thr Ile Pro Gln Gly Tyr Gly Ser Tyr Asn Ser Phe Ser
130 135 140

Ile Asn Tyr Lys Thr Lys Ile Thr Asn Glu Gln Gln Lys Glu Phe Val
145 150 155 160

Asn Asn Ser Gln Ala Trp Tyr Gln Glu His Gly Lys Glu Glu Val Asn
165 170 175

Gly Lys Ser Phe Asn His Thr Val His Asn Ile Asn Ala Asn Ala Gly
180 185 190

Ile Glu Gly Thr Val Lys Gly Glu Leu Lys Val Leu Lys Gln Asp Lys
195 200 205

Asp Thr Lys
210

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCACGAGATA TTTCATCAAC GAATGTTACA GATTTAACTG TATCACCGTC TAAGATAGAA	60
GATGGTGGTA AAACGACAGT AAAAATGACG TTCGACGATA AAAATGGAAA AATACAAAAT	120
GGTGACATGA TTAAAGTGGC ATGGCCGACA AGCGGTACAG TAAAGATAGA GGGTTATAGT	180
AAAACAGTAC CATTAACTGT TAAAGGTGAA CAGGTGGGTC AAGCAGTTAT TACACCAGAC	240
GGTGCAACAA TTACATTCAA TGATAAAGTA GAAAAATTAA GTGATGTTTC GGGATTTGCA	300
GAATTTGAAG TACAAGGAAG AAATTTAACG CAAACAAATA CTTCAGATGA CAAAGTAGCT	360
ACGATAACAT CTGGGAATAA ATCAACGAAT GTTACGGTTC ATAAAAGTGA AGCGGGAACA	420
AGTAGTGTTT TCTATTATAA AACGGGAGAT ATGCTACCAG AAGATACGAC ACATGTACGA	480
TGGTTTTTAA ATATTAACAA TGAAAAAAGT TATGTATCGA AAGATATTAC TATAAAGGAT	540
CAGATTCAAG GTGGACAGCA GTTAGATTTA AGCACATTAA ACATTAATGT GACAGGTACA	600
CATAGCAATT ATTATAGTGG ACAAAGTGCA ATTACTGATT TTGAAAAAGC CTTTCCAGGT	660
TCTAAAATAA CTGTTGATAA TACGAAGAAC ACAATTGATG TAACAATTCC ACAAGGCTAT	720
GGGTCATATA ATAGTTTTTC AATTA ACTAC AAAACCAAAA TTACGAATGA ACAGCAAAAA	780
GAGTTTGTTA ATAATTCACA AGCTTGGTAT CAAGAGCATG GTAAGGAAGA AGTGAACGGG	840
AAATCATTTA ATCATACTGT GCACAATATT AATGCTAATG CCGGTATTGA AGGTACTGTA	900
AAAGGTGAAT TAAAAGTTTT AAAACAGGAT AAAGATACCA AGGCTCCTAT AGCTAATGTA	960
AAATTTAAAC TTTCTAAAAA AGATGGATCA GTTGTAAGG ACAATCAAAA AGAAATTGAG	1020
ATTATAACAG ATGCAAACGG TATTGCTAAT ATTAAAGCGT TGCCTAGTGG AGACTATATT	1080
TTAAAAGAAA TAGAGGCGCC ACGACCGTAT ACATTTGATA AGGATAAAGA ATATCCGTTT	1140
ACTATGAAAG ATACAGATAA TCAGGGATAT TTTACGACTA TTGAAAATGC AAAAGCGATA	1200
GAAAAACAA AAGATGTTTC TGCTCAAAG GTTTGGGAAG GCACTCAAAA AGTGAAACCA	1260

ACGATTTATT TCAAGTTGTA CAAACAAGAT GACAATCAAA ATACAACACC AGTAGACAAA 1320
 GCAGAGATTA AAAAATTAGA AGATGGAACG ACAAAGTGA CATGGTCTAA TCTTCCGGAA 1380
 AATGACAAAA ATGGCAAGGC TATTAAATAT TTAGTTAAAG AAGTAAATGC TCAAGGTGAA 1440
 GATACAACAC CAGAAGGATA TACTAAAAAA GAAAATGGTT TAGTGGTTAC TAATACTGAA 1500

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Arg	Gly	Ser	His	His	His	His	His	Gly	Ser	Ala	Arg	Asp	Ile
1				5				10				15		
Ser	Ser	Thr	Asn	Val	Thr	Asp	Leu	Thr	Val	Ser	Pro	Ser	Lys	Ile
			20				25					30		Glu
Asp	Gly	Gly	Lys	Thr	Thr	Val	Lys	Met	Thr	Phe	Asp	Asp	Lys	Asn
		35					40				45			Gly
Lys	Ile	Gln	Asn	Gly	Asp	Met	Ile	Lys	Val	Ala	Trp	Pro	Thr	Ser
	50					55				60				Gly
Thr	Val	Lys	Ile	Glu	Gly	Tyr	Ser	Lys	Thr	Val	Pro	Leu	Thr	Val
65					70				75					80
Gly	Glu	Gln	Val	Gly	Gln	Ala	Val	Ile	Thr	Pro	Asp	Gly	Ala	Thr
			85					90					95	Ile
Thr	Phe	Asn	Asp	Lys	Val	Glu	Lys	Leu	Ser	Asp	Val	Ser	Gly	Phe
		100						105					110	Ala
Glu	Phe	Glu	Val	Gln	Gly	Arg	Asn	Leu	Thr	Gln	Thr	Asn	Thr	Ser
	115						120					125		Asp
Asp	Lys	Val	Ala	Thr	Ile	Thr	Ser	Gly	Asn	Lys	Ser	Thr	Asn	Val
	130					135				140				Thr
Val	His	Lys	Ser	Glu	Ala	Gly	Thr	Ser	Ser	Val	Phe	Tyr	Tyr	Lys
145					150				155					160
Gly	Asp	Met	Leu	Pro	Glu	Asp	Thr	Thr	His	Val	Arg	Trp	Phe	Leu
			165					170					175	Asn
Ile	Asn	Asn	Glu	Lys	Ser	Tyr	Val	Ser	Lys	Asp	Ile	Thr	Ile	Lys
														Asp

180	185	190
Gln Ile Gln Gly Gly Gln Gln Leu Asp Leu Ser Thr Leu Asn Ile Asn 195 200 205		
Val Thr Gly Thr His Ser Asn Tyr Tyr Ser Gly Gln Ser Ala Ile Thr 210 215 220		
Asp Phe Glu Lys Ala Phe Pro Gly Ser Lys Ile Thr Val Asp Asn Thr 225 230 235 240		
Lys Asn Thr Ile Asp Val Thr Ile Pro Gln Gly Tyr Gly Ser Tyr Asn 245 250 255		
Ser Phe Ser Ile Asn Tyr Lys Thr Lys Ile Thr Asn Glu Gln Gln Lys 260 265 270		
Glu Phe Val Asn Asn Ser Gln Ala Trp Tyr Gln Glu His Gly Lys Glu 275 280 285		
Glu Val Asn Gly Lys Ser Phe Asn His Thr Val His Asn Ile Asn Ala 290 295 300		
Asn Ala Gly Ile Glu Gly Thr Val Lys Gly Glu Leu Lys Val Leu Lys 305 310 315 320		
Gln Asp Lys Asp Thr Lys Ala Pro Ile Ala Asn Val Lys Phe Lys Leu 325 330 335		
Ser Lys Lys Asp Gly Ser Val Val Lys Asp Asn Gln Lys Glu Ile Glu 340 345 350		
Ile Ile Thr Asp Ala Asn Gly Ile Ala Asn Ile Lys Ala Leu Pro Ser 355 360 365		
Gly Asp Tyr Ile Leu Lys Glu Ile Glu Ala Pro Arg Pro Tyr Thr Phe 370 375 380		
Asp Lys Asp Lys Glu Tyr Pro Phe Thr Met Lys Asp Thr Asp Asn Gln 385 390 395 400		
Gly Tyr Phe Thr Thr Ile Glu Asn Ala Lys Ala Ile Glu Lys Thr Lys 405 410 415		
Asp Val Ser Ala Gln Lys Val Trp Glu Gly Thr Gln Lys Val Lys Pro 420 425 430		
Thr Ile Tyr Phe Lys Leu Tyr Lys Gln Asp Asp Asn Gln Asn Thr Thr 435 440 445		
Pro Val Asp Lys Ala Glu Ile Lys Lys Leu Glu Asp Gly Thr Thr Lys 450 455 460		

Val Thr Trp Ser Asn Leu Pro Glu Asn Asp Lys Asn Gly Lys Ala Ile
 465 470 475 480

Lys Tyr Leu Val Lys Glu Val Asn Ala Gln Gly Glu Asp Thr Thr Pro
 485 490 495

Glu Gly Tyr Thr Lys Lys Glu Asn Gly Leu Val Val Thr Asn Thr Glu
 500 505 510

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Arg Gly Ser His His His His His His Gly Ser Met Val Ala Ala
 1 5 10 15

Asp Ala Pro Ala Ala Gly Thr Asp Ile Thr Asn Gln Leu Thr Asn Val
 20 25 30

Thr Val Gly Ile Asp Ser Gly Thr Thr Val Tyr Pro His Gln Ala Gly
 35 40 45

Tyr Val Lys Leu Asn Tyr Gly Phe Ser Val Pro Asn Ser Ala Val Lys
 50 55 60

Gly Asp Thr Phe Lys Ile Thr Val Pro Lys Glu Leu Asn Leu Asn Gly
 65 70 75 80

Val Thr Ser Thr Ala Lys Val Pro Pro Ile Met Ala Gly Asp Gln Val
 85 90 95

Leu Ala Asn Gly Val Ile Asp Ser Asp Gly Asn Val Ile Tyr Thr Phe
 100 105 110

Thr Asp Tyr Val Asn Thr Lys Asp Asp Val Lys Ala Thr Leu Thr Met
 115 120 125

Pro Ala Tyr Ile Asp Pro Glu Asn Val Lys Lys Thr Gly Asn Val Thr
 130 135 140

Leu Ala Thr Gly Ile Gly Ser Thr Thr Ala Asn Lys Thr Val Leu Val
 145 150 155 160

Asp Tyr Glu Lys Tyr Gly Lys Phe Tyr Asn Leu Ser Ile Lys Gly Thr
 165 170 175

Ile	Asp	Gln	Ile	Asp	Lys	Thr	Asn	Asn	Thr	Tyr	Arg	Gln	Thr	Ile	Tyr	180	185	190
Val	Asn	Pro	Ser	Gly	Asp	Asn	Val	Ile	Ala	Pro	Val	Leu	Thr	Gly	Asn	195	200	205
Leu	Lys	Pro	Asn	Thr	Asp	Ser	Asn	Ala	Leu	Ile	Asp	Gln	Gln	Asn	Thr	210	215	220
Ser	Ile	Lys	Val	Tyr	Lys	Val	Asp	Asn	Ala	Ala	Asp	Leu	Ser	Glu	Ser	225	230	235
Tyr	Phe	Val	Asn	Pro	Glu	Asn	Phe	Glu	Asp	Val	Thr	Asn	Ser	Val	Asn	245	250	255
Ile	Thr	Phe	Pro	Asn	Pro	Asn	Gln	Tyr	Lys	Val	Glu	Phe	Asn	Thr	Pro	260	265	270
Asp	Asp	Gln	Ile	Thr	Thr	Pro	Tyr	Ile	Val	Val	Val	Asn	Gly	His	Ile	275	280	285
Asp	Pro	Asn	Ser	Lys	Gly	Asp	Leu	Ala	Leu	Arg	Ser	Thr	Leu	Tyr	Gly	290	295	300
Tyr	Asn	Ser	Asn	Ile	Ile	Trp	Arg	Ser	Met	Ser	Trp	Asp	Asn	Glu	Val	305	310	315
Ala	Phe	Asn	Asn	Gly	Ser	Gly	Ser	Gly	Asp	Gly	Ile	Asp	Lys	Pro	Val	325	330	335
Val	Pro	Glu	Gln	Pro	Asp	Glu	Gln	Ala								340	345	

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Arg	Gly	Ser	His	His	His	His	His	His	Gly	Ser	Glu	Gly	Gly	Gln	1	5	10	15
Asn	Ser	Gly	Asn	Gln	Ser	Phe	Glu	Glu	Asp	Thr	Glu	Glu	Asp	Lys	Pro	20	25	30	
Lys	Tyr	Glu	Gln	Gly	Gly	Asn	Ile	Val	Asp	Ile	Asp	Phe	Asp	Ser	Val	35	40	45	

Ser Gly Gln Asn Glu Phe Asp Ile Lys Leu Asn
130 135

[illegible]